

SEQUENCE LISTING

<110> TRANSGENE SA et al.

<120> MUC-1 derived peptides

<130> D 2195 US

<140>

<141>

<160> 67

<170> PatentIn Ver. 2.1

<210> 1

<211> 1572

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)..(1542)

<400> 1

gaattccctg gctgcttgaa tctgttctgc cccctcccca cccatttcac caccacc 57

atg aca ccg ggc acc cag tct cct ttc ttc ctg ctg ctg ctc ctc aca 105

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
1 5 10 15

gtg ctt aca gtt gtt aca ggt tct ggt cat gca agc tct acc cca ggt 153

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

gga gaa aag gag act tcg gct acc cag aga agt tca gtg ccc agc tct 201

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

act gag aag aat gct gtg agt atg acc agc agc gta ctc tcc agc cac 249

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
50 55 60

agc ccc ggt tca ggc tcc tcc acc act cag gga cag gat gtc act ctg 297

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65 70 75 80

gcc ccg gcc acg gaa cca gct tca ggt tca gct gcc acc tgg gga cag 345

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
85 90 95

gat gtc acc tcg gtc cca gtc acc agg cca gcc ctg ggc tcc acc acc 393

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100 105 110

ccg cca gcc cac gat gtc acc tca gcc ccg gac aac aag cca gcc ccg 441

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
115 120 125

ggc tcc acc gcc ccc ccg gcc cac ggt gtc acc tcg gcc ccg gac acc 489

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
130 135 140

000001.12000000

agg ccg ccc ccg ggc tcc acc gcc ccc gcc gcc cac ggt gtc acc tcg 537
 Arg Pro Pro Gly Ser Thr Ala Pro Ala Ala His Gly Val Thr Ser
 145 150 155 160

gcc ccg gac acc agg ccg gcc ccg ggc tcc acc gcc ccc ccg gcc cac 585
 Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
 165 170 175

ggt gtc acc tcg gcc ccg gac aac agg ccg gcc ttg ggc tcc acc gcc 633
 Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala
 180 185 190

cct cca gtc cac aat gtc acc tcg gcc tca ggc tct gca tca ggc tca 681
 Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser
 195 200 205

gct tct act ctg gtg cac aac gcc acc tct gcc agg gct acc aca acc 729
 Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr
 210 215 220

cca gcc agc aag agc act cca ccc agc att ccc agc cac cac tct gat 777
 Pro Val Ala Ser Lys Ser Thr Pro Pro Ser Ile Pro Ser His His Ser Asp
 225 230 235 240

act cct acc acc ctt gcc agc cat agc acc aag act gat gcc agt agc 825
 Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser
 245 250 255

act cac cat agc acg gta cct cct ctc acc tcc tcc aat cac agc act 873
 Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr
 260 265 270

tct ccc cag ttg tct act ggg gtc tct ttc ttc ttc ctg tct ttt cac 921
 Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His
 275 280 285

att tca aac ctc cag ttt aat tcc tct ctg gaa gat ccc agc acc gac 969
 Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
 290 295 300

tac tac caa gag ctg cag aga gac att tct gaa atg ttt ttg cag att 1017
 Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
 305 310 315 320

tat aaa caa ggg ggt ttt ctg gcc ctc tcc aat att aag ttc agg cca 1065
 Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
 325 330 335

gga tct gtg gtg gta caa ttg act cgg gcc ttc cga gaa ggt acc atc 1113
 Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile
 340 345 350

aat gtc cac gac gtg gag aca cag ttc aat cag tat aaa acg gaa gca 1161
 Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
 355 360 365

gcc tct cga tat aac ctg acg etc tca gac gtc agc gtg agt cat gtg 1209
 Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser His Val
 370 375 380

cca ttt cct ttc tct gcc cag tct ggg gct ggg gtg cca ggc tgg ggc 1257
 Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly
 385 390 395 400

09553621.090600

atc gcg ctg ctg gtg ctg gtc tgt gtt ctg gtt gcg ctg gcc att gtc 1305
 Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu Ala Ile Val
 405 410 415
 tat ctc att gcc ttg gct gtc tgt cag tgc cgc cga aag aac tac ggg 1353
 Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly
 420 425 430
 cag ctg gac atc ttt cca gcc cgg gat acc tac cat cct atg agc gag 1401
 Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu
 435 440 445
 tac ccc acc tac cac acc cat ggg cgc tat gtg ccc cct agc agt acc 1449
 Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Ser Ser Thr
 450 455 460
 gat cgt agc ccc tat gag aag gtt tct gca ggt aat ggt ggc agc agc 1497
 Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser
 465 470 475 480
 ctc tct tac aca aac cca gca gtg gca gcc act tct gcc aac ttg 1542
 Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
 485 490 495
 taggggcacg tcgccctctg agctgagtg 1572

 <210> 2
 <211> 495
 <212> PRT
 <213> Homo sapiens

 <400> 2
 Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
 1 5 10 15
 Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30
 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45
 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60
 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80
 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95
 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110
 Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115 120 125
 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130 135 140
 Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His Gly Val Thr Ser
 145 150 155 160

00553321-000000

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
165 170 175

Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala
180 185 190

Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser
195 200 205

Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr
210 215 220

Pro Ala Ser Lys Ser Thr Pro Pro Ser Ile Pro Ser His His Ser Asp
225 230 235 240

Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser
245 250 255

Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr
260 265 270

Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His
275 280 285

Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
290 295 300

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
305 310 315 320

Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
325 330 335

Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile
340 345 350

Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
355 360 365

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser His Val
370 375 380

Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly
385 390 395 400

Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu Ala Ile Val
405 410 415

Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly
420 425 430

Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu
435 440 445

Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr
450 455 460

Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser
465 470 475 480

Leu Ser Tyr Thr Asn Pro Ala Val Ala Thr Ser Ala Asn Leu
485 490 495

00650621.090800

<210> 3
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> CDS
<222> (58)..(1542)

<400> 3
Ala Leu Gly Ser Thr Ala Pro Pro Val
1 5

<210> 4
<211> 9
<212> PRT
<213> Homo sapiens

<400> 4
Phe Leu Ser Phe His Ile Ser Asn Leu
1 5

<210> 5
<211> 9
<212> PRT
<213> Homo sapiens

<400> 5
Thr Leu Ala Pro Ala Thr Glu Pro Ala
1 5

<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6
Ser Leu Ser Tyr Thr Asn Pro Ala Val
1 5

<210> 7
<211> 9
<212> PRT
<213> Homo sapiens

<400> 7
Ser Val Pro Val Thr Arg Pro Ala Leu
1 5

<210> 8

09658661.090800

<211> 9
<212> PRT
<213> Homo sapiens

<400> 8
Gly Val Pro Gly Trp Gly Ile Ala Leu
1 5

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<400> 9
Ala Pro Gly Ser Thr Ala Pro Pro Ala
1 5

<210> 10
<211> 9
<212> PRT
<213> Homo sapiens

<400> 10
Ala Val Ser Met Thr Ser Ser Val Leu
1 5

<210> 11
<211> 9
<212> PRT
<213> Homo sapiens

<400> 11
Ala Val Ala Ala Thr Ser Ala Asn Leu
1 5

<210> 12
<211> 9
<212> PRT
<213> Homo sapiens

<400> 12
Arg Pro Gly Ser Val Val Val Gln Leu
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13
Val Pro Gly Trp Gly Ile Ala Leu Leu
1 5

008060-12985960

<210> 14
<211> 9
<212> PRT
<213> Homo sapiens

<400> 14
Ser Ala Ser Gly Ser Ala Ser Thr Leu
1 5

<210> 15
<211> 9
<212> PRT
<213> Homo sapiens

<400> 15
Ser Ala Gly Asn Gly Gly Ser Ser Leu
1 5

<210> 16
<211> 9
<212> PRT
<213> Homo sapiens

<400> 16
Ala Leu Ala Val Cys Gln Cys Arg Arg
1 5

<210> 17
<211> 9
<212> PRT
<213> Homo sapiens

<400> 17
Gly Gln Leu Asp Ile Phe Pro Ala Arg
1 5

<210> 18
<211> 10
<212> PRT
<213> Homo sapiens

<400> 18
Thr Leu Val His Asn Gly Thr Ser Ala Arg
1 5 10

<210> 19
<211> 9
<212> PRT
<213> Homo sapiens

<400> 19

008060-12955960

<400> 24
Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
1 5 10

<400> 25
Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser
1 5 10

<400> 26
Ile Ser Glu Met Phe Leu Gln Ile Tyr
1 5

```
<400> 27
Asp Val Glu Thr Gln Phe Asn Gln Tyr
  1             5
```

<400> 28
Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr
1 5 10

<400> 29
Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys
1 5 10

<400> 30
Asn Ile Lys Phe Arg Pro Gly Ser Val

0985671-09800

5

<400> 31
Thr Leu Ala Phe Arg Glu Gly Thr Ile
1 5

<400> 32
Gln Cys Arg Arg Lys Asn Tyr Gly Gln Leu
1 5 10

<400> 33
Glu Ala Ala Ser Arg Tyr Asn Leu Thr
1 5

```
<400> 34
gccttggggt ccaccgcccc tccagtc
```

<400> 35
ttcctgtctt ttcacatttc aaacctc

<400> 36
actctgcccc cggccacgga accagct

<400> 43
aggccaggat ctgtggtggt acaattg

```
<400> 50
accacccttg ccagccatag caccaag
```

27

```

<210> 51
<211> 27
<212> DNA
<213> Homo sapiens

<400> 51
ggtgtcacct cggccccgga caccagg                27

<210> 52
<211> 27
<212> DNA
<213> Homo sapiens

<400> 52
ggtgtcacct cggccccgga caacagg                27

<210> 53
<211> 30
<212> DNA
<213> Homo sapiens

<400> 53
atttataaac aaggggggtt tctgggcctc                30

<210> 54
<211> 30
<212> DNA
<213> Homo sapiens

<400> 54
tttttctgt cttttcacat ttcaaacctc                30

<210> 55
<211> 30
<212> DNA
<213> Homo sapiens

<400> 55
ggttttctgg gcctctccaa tattaagttc                30

<210> 56
<211> 30
<212> DNA
<213> Homo sapiens

<400> 56
tactaccaag agctgcagag agacatttct                30

<210> 57
<211> 27
<212> DNA
<213> Homo sapiens

<400> 57
atttctgaaa tqtttttcca gatttat                27

```

<210> 58
<211> 30
<212> DNA
<213> Homo sapiens

<400> 58
attttctgaaa tgtttttgca gatttataaa

30

<210> 59
<211> 30
<212> DNA
<213> Homo sapiens

<400> 59
tctcttgaag atcccagcac cgactactac

30

<210> 60
<211> 27
<212> DNA
<213> Homo sapiens

<400> 60
gacgtggaga cacagttcaa tcagtat

27

<210> 61
<211> 27
<212> DNA
<213> Homo sapiens

<400> 61
aatattaagt tcaggccagg atctgtg

27

<210> 62
<211> 27
<212> DNA
<213> Homo sapiens

<400> 62
actctggcct tccgagaagg tagcatc

27

<210> 63
<211> 30
<212> DNA
<213> Homo sapiens

<400> 63
cagtgccgcc gaaagaacta cgggcagctg

30

<210> 64
<211> 27
<212> DNA
<213> Homo sapiens

<400> 64
gaagcagcct ctccgatataa cctgacg

27

00000012985960

<210> 65
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 65
 Leu Leu Leu Thr Val Leu Thr Val Val
 1 5

<210> 66
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 66
 Ala Leu Gly Ser Thr Thr Pro Pro Ala
 1 5

<210> 67
 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 1
 Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
 1 5 10 15
 Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30
 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45
 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60
 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80
 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95
 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110
 Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115 120 125
 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130 135 140
 Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145 150 155 160
 Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His
 165 170 175
 Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
 180 185 190
 Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys

000000.1292590

1

1